STIC Biotechnology Systems Branch
RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/555, 583_
Source: _PCT_
Date Processed by STIC: _12/01/2005_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT,

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
> http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
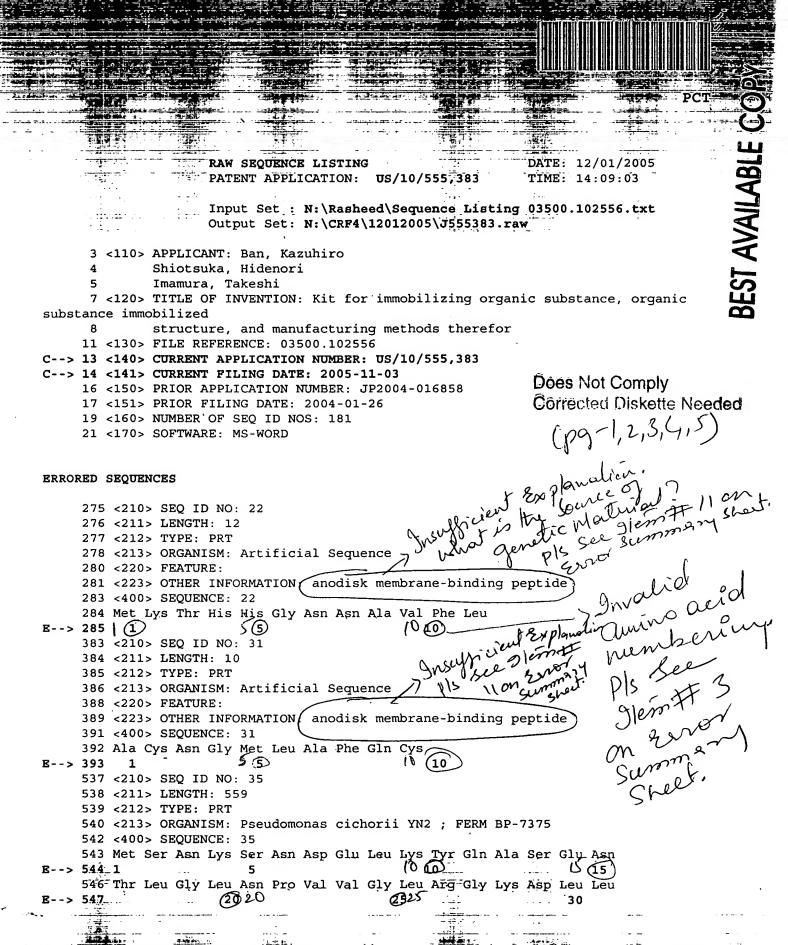Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/533,583

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to "3"; this will prevent "wrapping."

2 ____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length — Sequence(s) ____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ____ Skipped Sequences (OLD RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 ____ Skipped Sequences (NEW RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220> — Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa — "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

PCT

```
    RAW SEQUENCE LISTING                          DATE: 12/01/2005
    PATENT APPLICATION:   US/10/555,383          TIME: 14:09:03

    Input Set : N:\Rasheed\Sequence Listing 03500.102556.txt
    Output Set: N:\CRF4\12012005\J555383.raw
```

```
      3 <110> APPLICANT: Ban, Kazuhiro
      4         Shiotsuka, Hidenori
      5         Imamura, Takeshi
      7 <120> TITLE OF INVENTION: Kit for immobilizing organic substance, organic
substance immobilized
      8         structure, and manufacturing methods therefor
     11 <130> FILE REFERENCE: 03500.102556
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/555,383
C--> 14 <141> CURRENT FILING DATE: 2005-11-03
     16 <150> PRIOR APPLICATION NUMBER: JP2004-016858
     17 <151> PRIOR FILING DATE: 2004-01-26
     19 <160> NUMBER OF SEQ ID NOS: 181
     21 <170> SOFTWARE: MS-WORD
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Does Not Comply
Corrected Diskette Needed

(pg-1,2,3,4,5)

ERRORED SEQUENCES

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    275 <210> SEQ ID NO: 22
    276 <211> LENGTH: 12
    277 <212> TYPE: PRT
    278 <213> ORGANISM: Artificial Sequence
    280 <220> FEATURE:
    281 <223> OTHER INFORMATION  anodisk membrane-binding peptide
    283 <400> SEQUENCE: 22
    284 Met Lys Thr His His Gly Asn Asn Ala Val Phe Leu
E--> 285 |  1                    5  5              10  10
    383 <210> SEQ ID NO: 31
    384 <211> LENGTH: 10
    385 <212> TYPE: PRT
    386 <213> ORGANISM: Artificial Sequence
    388 <220> FEATURE:
    389 <223> OTHER INFORMATION  anodisk membrane-binding peptide
    391 <400> SEQUENCE: 31
    392 Ala Cys Asn Gly Met Leu Ala Phe Gln Cys
E--> 393    1                   5  5              10  10
    537 <210> SEQ ID NO: 35
    538 <211> LENGTH: 559
    539 <212> TYPE: PRT
    540 <213> ORGANISM: Pseudomonas cichorii YN2 ; FERM BP-7375
    542 <400> SEQUENCE: 35
    543 Met Ser Asn Lys Ser Asn Asp Glu Leu Lys Tyr Gln Ala Ser Gly Asn
E--> 544 1                   5                  10  10             15  15
    546 Thr Leu Gly Leu Asn Pro Val Val Gly Leu Arg Gly Lys Asp Leu Leu
E--> 547                     20 20                23 25              30
```

Insufficient Explanation.
what is the source of
genetic Material?
Pls see gleim # 11 on
Error summary sheet.

Invalid
amino acid
numbering
Pls see
gleim # 3
on Error
Summary
Sheet.

Insufficient Explanation
Pls see gleim #
11 on Error
Summary
sheet.

```
                    RAW SEQUENCE LISTING                    DATE: 12/01/2005
                PATENT APPLICATION: US/10/555,383          TIME: 14:09:03

              Input Set: N:\Rasheed\Sequence Listing 03500.102556.txt
              Output Set: N:\CRF4\12012005\J555383.raw

        549 Ala Ser Ala Arg Met Val Leu Arg Gln Ala Ile Lys Gln Pro Val His
E--> 550           35              40                    45
        552 Ser Val Lys His Val Ala His Phe Gly Leu Glu Leu Lys Asn Val Leu
E--> 553           50              55                    60
        555 Leu Gly Lys Ser Gly Leu Gln Pro Thr Ser Asp Asp Arg Arg Phe Ala
E--> 556 65              70              75                          80
        558 Asp Pro Ala Trp Ser Gln Asn Pro Leu Tyr Lys Arg Tyr Leu Gln Thr
E--> 559 80              85                    90                    95
        561 Tyr Leu Ala Trp Arg Lys Glu Leu His Asp Trp Ile Asp Glu Ser Asn
E--> 562           100             105                   110
        564 Leu Ala Pro Lys Asp Val Ala Arg Gly His Phe Val Ile Asn Leu Met
E--> 565           115             120                   125
        567 Thr Glu Ala Met Ala Pro Thr Asn Thr Ala Ala Asn Pro Ala Ala Val
        568      130                 135                   140
        570 Lys Arg Phe Phe Glu Thr Gly Gly Lys Ser Leu Leu Asp Gly Leu Ser
E--> 571 145                150                   155                   160
        573 His Leu Ala Lys Asp Leu Val His Asn Gly Gly Met Pro Ser Gln Val
E--> 574                165                   170                   175
        576 Asn Met Gly Ala Phe Glu Val Gly Lys Ser Leu Gly Val Thr Glu Gly
E--> 577                180                   185                   190
        579 Ala Val Val Phe Arg Asn Asp Val Leu Glu Leu Ile Gln Tyr Lys Pro
E--> 580           195                   200                   205
        582 Thr Thr Glu Gln Val Tyr Glu Arg Pro Leu Leu Val Val Pro Pro Gln
E--> 583           210                   215                   220
        585 Ile Asn Lys Phe Tyr Val Phe Asp Leu Ser Pro Asp Lys Ser Leu Ala
        586 225                230                   235                   240
        588 Arg Phe Cys Leu Arg Asn Asn Val Gln Thr Phe Ile Val Ser Trp Arg
E--> 589                245                   250                   255
        591 Asn Pro Thr Lys Glu Gln Arg Glu Trp Gly Leu Ser Thr Tyr Ile Glu
E--> 592                260                   265                   270
        594 Ala Leu Lys Glu Ala Val Asp Val Val Thr Ala Ile Thr Gly Ser Lys
E--> 595           275                   280                   285
        597 Asp Val Asn Met Leu Gly Ala Cys Ser Gly Gly Ile Thr Cys Thr Ala
E--> 598      290                 295                   300
        600 Leu Leu Gly His Tyr Ala Ala Ile Gly Glu Asn Lys Val Asn Ala Leu
        601 305                 310                   315                   320
        603 Thr Leu Leu Val Ser Val Leu Asp Thr Thr Leu Asp Ser Asp Val Ala
E--> 604                325                   330                   335
        606 Leu Phe Val Asn Glu Gln Thr Leu Glu Ala Ala Lys Arg His Ser Tyr
E--> 607           340                   345                   350
        609 Gln Ala Gly Val Leu Glu Gly Arg Asp Met Ala Lys Val Phe Ala Trp
E--> 610           355                   360                   365
        612 Met Arg Pro Asn Asp Leu Ile Trp Asn Tyr Trp Val Asn Asn Tyr Leu
E--> 613      370                 375                   380
        615 Leu Gly Asn Glu Pro Pro Val Phe Asp Ile Leu Phe Trp Asn Asn Asp
E--> 616 385                390                   395                   400
        618 Thr Thr Arg Leu Pro Ala Ala Phe His Gly Asp Leu Ile Glu Leu Phe
E--> 619                405                   410                   415
        621 Lys Asn Asn Pro Leu Ile Arg Pro Asn Ala Leu Glu Val Cys Gly Thr
```

```
E--> 622                420                 425                      430
     624 Pro Ile Asp Leu Lys Gln Val Thr Ala Asp Ile Phe Ser Leu Ala Gly
     625          435              440                445
     627 Thr Asn Asp His Ile Thr Pro Trp Lys Ser Cys Tyr Lys Ser Ala Gln
     628     450              455                  460
     630 Leu Phe Gly Gly Asn Val Glu Phe Val Leu Ser Ser Ser Gly His Ile
E--> 631 465                 470              475                     480
     633 Gln Ser Ile Leu Asn Pro Pro Gly Asn Pro Lys Ser Arg Tyr Met Thr
E--> 634                485                 490                     495
     636 Ser Thr Glu Val Ala Glu Asn Ala Asp Glu Trp Gln Ala Asn Ala Thr
E--> 637          500                 505                 510
     639 Lys His Thr Asp Ser Trp Trp Leu His Trp Gln Ala Trp Gln Ala Gln
E--> 640          515                 520                 525
     642 Arg Ser Gly Glu Leu Lys Lys Ser Pro Thr Lys Leu Gly Ser Lys Ala
E--> 643          530                 535                 540
     645 Tyr Pro Ala Gly Glu Ala Ala Pro Gly Thr Tyr Val His Glu Arg
     646 545                 550                 555
     648 <210> SEQ ID NO: 36
     649 <211> LENGTH: 560
     650 <212> TYPE: PRT
     651 <213> ORGANISM: Pseudomonas cichorii YN2 ; FERM BP-7375
     653 <400> SEQUENCE: 36
     654 Met Arg Asp Lys Pro Ala Arg Glu Ser Leu Pro Thr Pro Ala Lys Phe
     655 1                5                   10                  15
     657 Ile Asn Ala Gln Ser Ala Ile Thr Gly Leu Arg Gly Arg Asp Leu Val
     658          20                  25                  30
     660 Ser Thr Leu Arg Ser Val Ala Ala His Gly Leu Arg His Pro Val His
E--> 661          35                  40                  45
     663 Thr Ala Arg His Ala Leu Lys Leu Gly Gly Gln Leu Gly Arg Val Leu
E--> 664     50                  55                      60
     666 Leu Gly Asp Thr Leu His Pro Thr Asn Pro Gln Asp Arg Arg Phe Asp
E--> 667 65                  70                  75                      80
     669 Asp Pro Ala Trp Ser Leu Asn Pro Phe Tyr Arg Arg Ser Leu Gln Ala
E--> 670              85                  90                      95
     672 Tyr Leu Ser Trp Gln Lys Gln Val Lys Ser Trp Ile Asp Glu Ser Asn
     673              100                 105                 110
     675 Met Ser Pro Asp Asp Arg Ala Arg Ala His Phe Ala Phe Ala Leu Leu
E--> 676          115                 120                 125
     678 Asn Asp Ala Val Ser Pro Ser Asn Ser Leu Leu Asn Pro Leu Ala Ile
E--> 679     130                 135                 140
     681 Lys Glu Ile Phe Asn Ser Gly Gly Asn Ser Leu Val Arg Gly Ile Gly
     682 145                 150                 155                 160
     684 His Leu Val Asp Asp Leu Leu His Asn Asp Gly Leu Pro Arg Gln Val
E--> 685                165                 170                 175
     687 Thr Arg His Ala Phe Glu Val Gly Lys Thr Val Ala Thr Thr Thr Gly
E--> 688          180                 185                 190
     690 Ala Val Val Phe Arg Asn Glu Leu Leu Glu Leu Ile Gln Tyr Lys Pro
E--> 691          195                 200                 205
     693 Met Ser Glu Lys Gln Tyr Ser Lys Pro Leu Leu Val Val Pro Pro Gln
```

Saint Error

RAW SEQUENCE LISTING DATE: 12/01/2005
PATENT APPLICATION: US/10/555,383 TIME: 14:09:03

Input Set: N:\Rasheed\Sequence Listing 03500.102556.txt
Output Set: N:\CRF4\12012005\J555383.raw

```
E--> 694        210                  215                  220
     696 Ile Asn Lys Tyr Tyr Ile Phe Asp Leu Ser Pro His Asn Ser Phe Val
     697 225                  230                  235                  240
     699 Gln Phe Ala Leu Lys Asn Gly Leu Gln Thr Phe Val Ile Ser Trp Arg
E--> 700                  245                  250                  255
     702 Asn Pro Asp Val Arg His Arg Glu Trp Gly Leu Ser Thr Tyr Val Glu
E--> 703                  260                  265                  270
     705 Ala Val Glu Glu Ala Met Asn Val Cys Arg Ala Ile Thr Gly Ala Arg
E--> 706                  275                  280                  285
     708 Glu Val Asn Leu Met Gly Ala Cys Ala Gly Gly Leu Thr Ile Ala Ala
E--> 709                  290                  295                  300
     711 Leu Gln Gly His Leu Gln Ala Lys Arg Gln Leu Arg Arg Val Ser Ser
E--> 712 305                  310                  315                  320
     714 Ala Thr Tyr Leu Val Ser Leu Leu Asp Ser Gln Leu Asp Ser Pro Ala
E--> 715                  325                  330                  335
     717 Thr Leu Phe Ala Asp Glu Gln Thr Leu Glu Ala Ala Lys Arg Arg Ser
E--> 718                  340                  345                  350
     720 Tyr Gln Lys Gly Val Leu Glu Gly Arg Asp Met Ala Lys Val Phe Ala
E--> 721                  355                  360                  365
     723 Trp Met Arg Pro Asn Asp Leu Ile Trp Ser Tyr Phe Val Asn Asn Tyr
E--> 724                  370                  375                  380
     726 Leu Met Gly Lys Glu Pro Pro Ala Phe Asp Ile Leu Tyr Trp Asn Asn
E--> 727 385                  390                  395                  400
     729 Asp Asn Thr Arg Leu Pro Ala Ala Leu His Gly Asp Leu Leu Asp Phe
E--> 730                  405                  410                  415
     732 Phe Lys His Asn Pro Leu Ser His Pro Gly Gly Leu Glu Val Cys Gly
E--> 733                  420                  425                  430
     735 Thr Pro Ile Asp Leu Gln Lys Val Thr Val Asp Ser Phe Ser Val Ala
     736                  435                  440                  445
     738 Gly Ile Asn Asp His Ile Thr Pro Trp Asp Ala Val Tyr Arg Ser Thr
     739 450                  455                  460
     741 Leu Leu Leu Gly Gly Glu Arg Arg Phe Val Leu Ala Asn Ser Gly His
E--> 742 465                  470                  475                  480
     744 Val Gln Ser Ile Leu Asn Pro Pro Asn Asn Pro Lys Ala Asn Tyr Leu
E--> 745                  485                  490                  495
     747 Glu Gly Ala Lys Leu Ser Ser Asp Pro Arg Ala Trp Tyr Tyr Asp Ala
E--> 748                  500                  505                  510
     750 Lys Pro Val Asp Gly Ser Trp Trp Thr Gln Trp Leu Gly Trp Ile Gln
E--> 751                  515                  520                  525
     753 Glu Arg Ser Gly Ala Gln Lys Glu Thr His Met Ala Leu Gly Asn Gln
E--> 754                  530                  535                  540
     756 Asn Tyr Pro Pro Met Glu Ala Ala Pro Gly Thr Tyr Val Arg Val Arg
     757 545                  550                  555                  560
    2390 <210> SEQ ID NO: 172
    2391 <211> LENGTH: 16
    2392 <212> TYPE: PRT
    2393 <213> ORGANISM: Artificial Sequence
    2395 <220> FEATURE:
    2396 <223> OTHER INFORMATION: anodisk membrane-binding peptide
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Same Error

Same Error.

Input Set : N:\Rasheed\Sequence Listing 03500:102556 txt
Output Set : N:\CRF4\12012005\J555383.raw

```
      2398  <400> SEQUENCE: 172
      2399  Val Tyr Ala Asn Gln Thr Pro Pro Ser Arg Ala Arg Ala Lys Ala Arg
E-->  2400   1               5                10                    15

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      2403  <211> LENGTH: 20
      2404  <212> TYPE: PRT
      2405  <213> ORGANISM: Artificial Sequence
      2407  <220> FEATURE:
      2408  <223> OTHER INFORMATION: anodisk membrane-binding peptide
      2410  <400> SEQUENCE: 173
      2411  Val Tyr Ala Asn Gln Thr Pro Pro Ser Lys Ala Arg Tyr Ala Gln
E-->  2412   1               5                10                    15
      2413  Thr Pro Pro Ser Arg
      2414                  20
```

Same Error

*Line of errors shown exist thr...
...nce Listing. Please check a...
sequences for similar errors.*

VERIFICATION SUMMARY   DATE: 12/01/2005
PATENT APPLICATION   US/10/555,383   TIME: 14:09:04

Input Set: N:\Rasheed\Sequence Listing 03500-102556.txt
Output Set: N:\CRF4\12012005\J555383.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application
Number.
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:285 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:393 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:31
L:411 M:283 W: Missing Blank Line separator, <220> field identifier
L:475 M:283 W: Missing Blank Line separator, <220> field identifier
L:544 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
L:547 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
L:550 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
L:553 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
L:556 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
L:559 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
L:562 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
L:565 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
L:571 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
L:574 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
L:577 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
L:580 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
L:583 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
L:589 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
L:592 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
L:595 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
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L:607 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
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L:616 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
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L:643 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
L:661 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:664 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:667 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:670 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:676 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:679 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:685 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:688 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:691 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:694 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:700 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:703 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:706 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36

Input Set: N:\Rasheed\Sequence Listing-03500102556.txt
Output Set: N:\CRF4\12012005\J555383.raw

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  L:712 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
  L:715 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
  L:718 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
  L:721 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
  L:724 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
  L:727 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
  L:730 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
  L:733 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
  L:742 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
  L:745 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
  L:748 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
  L:751 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
  L:754 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
  L:2400 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:172
  L:2412 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:173
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